

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: FALB, DEAN A.
- (ii) TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE
- (iii) NUMBER OF SEQUENCES: 38
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: PENNIE & EDMONDS
 - (B) STREET: 1155 Avenue of the Americas
 - (C) CITY: New York
 - (D) STATE: New York
 - (E) COUNTRY: USA
 - (F) ZIP: 10036-2711
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/485,573
 - (B) FILING DATE: 07-JUN-1995
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/386,844
 - (B) FILING DATE: 10-FEB-1995
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Coruzzi, Laura A.
 - (B) REGISTRATION NUMBER: 30,742
 - (C) REFERENCE/DOCKET NUMBER: 7853-032
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 - (C) TELEX: 66141 PENNIE

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 288 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGCTTAGATG CAGCCTGCAA ATTAACTTT GATTTTTCAT CTTGTGAAAG CAGTCCTTGT	60
TCCTATGGCC TAATGAACAA CTTCCAGGTA ATGAGTATGG TGTCAGGATT TACACCACTA	120

ATTTCTGCAG GTATATTTTC AGCCACTCTT TCTTCAGCAT TAGCATCCCT AGTGAGTGCT 180
 CCCAAAATAT TTCAGGCTCT ATGTAAGGAC AACATCTACC CAGCTTTCCA GATGTTTGCT 240
 AAAGGTTATG GGAAAAATAA TGAACCTCTT CGTGGCTGCA TCTAAGCC 288

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 178 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

AAAAATAAAT AAATTAAAGT CTGAGACCAA TTTGCCACTG TGAATATAAG CACATTAACC 60
 CCAGGAGGAG CCAAGAATA CACAAACCTC TCTATGAGAA TTTACCAGTC TTCTTTCATT 120
 TGGCAAGAAA AAGCTCAGGA AAATTTGCTT GTTTAAATTC TATGAGCCTA GTCTATGG 178

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 101 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGGTAATTCA TTAATTACAC TTATAAATTG GAAAGTGGGA TAAGAAATCT AAAGTAAACC 60
 AGCTTATCTT TGAAACAATA TTATTTTGAA ATTGGCTTTA A 101

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 184 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GGCTTGGTGG TGATGCCTAC AAGAAATGTT TACATACAAA CACTCTATAC ATCTAACTCC 60
CGAAAAAGGA CCAGCTATTT CGGCAACAGA AAAAAGACAA GCATTTTCAGA GGAGCGTTGC 120
TTTCCTTAAA GACCTAACTC ACTTAAGTCT TACAAACAGA AATAACAAGG AGGACAATTT 180
TCTA 184

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 284 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CTTGGGGATG CTGTTTGGAG GAATCCTCAT GAAGCGCTTT GTTTTCTCTC TACAAGCCAT 60
TCCCCGCATA GCTACCACCA TCATCACCAT CTCCATGATC CTTTGTGTTC CTTTGTCTT 120
CATGGGATGC TCCACCCCAA CTGTGGCCGA AGTCTACCCC CCTAGCACAT CAAGTTCTAT 180
ACATCCGCAG TCTCCTGCCT GCCGCAGGGA CTGCTCGTGC CCAGATTCTA TCTTCCACCC 240
GGTCTGTGGA GACAATGGAA TCGAGTACCT CTCCCCTTGC CATG 284

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2582 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GGCTTACCAT CGATGCGGCC GCGGATCCAG GGCTCAGAGG GAGGACGCAC CCGCCAGCCA 60
GCCGGGAACC TTCCCTCGCG GGCTCCCAGG GCGGGTCTCT TCCTCTCTCT AGCCCTGCTC 120
AGGCATTCCG CAGGTCCAGC AGAGGTACAC CTCCTGCAGC GGGTTCCAAG TGCACCTCCA 180
GCCTGATGGA CCTGACCAAG GAGGCTTCCA GGAGCACAGA AGGGGCTGCA ACCCAGGTAC 240
CCAGAGAGTG AGCAGCTCCA CGCGGGACTG TGCACGGTGG CCGACACCCG CAGGGACGCC 300
CACCGGACGA GCACGCGGAG GGCCCTCGCC TCCACGGATG CACCATGCCG GTGTGAGGAG 360
CATCTGTTCT TCCCCTCTC TGCAGTTAAC AAACCAACC CAAACCACCA CAGGTGCTCC 420
TCCTGGGGAG TTTCTGTCT GACAAATGCC AGGCTCACTT CAAGGAGAAT CACGCTTCTT 480

TCTAAAGATG	GATTCAACAT	TTAAAAACAGA	GCTCTGGGAG	CCTTTCGGCA	AATCTTGAAA	540
GCTGCACGGC	GCAGAGACAT	GGATGTGACT	TCCCAAGCCC	GGGGCGTAGG	CCTGGAGATG	600
TACCCAGGCA	CCGCGCAGCC	TGCGGCCCCC	AACACCACCT	CCCCCGAGCT	CAACCTGTCC	660
CACCCGCTCC	TGGGCACCGC	CCTGGCCAAT	GGGACAGGTG	AGCTCTCGGA	GCACCAGCAA	720
TACGTGATCG	GCCTGTTCTT	CTCGTGCCCT	TACACCATCT	TCCTCTTCCC	CATCGGCTTT	780
GTGGGCAACA	TCCTGATCCT	GGTGGTGAAC	ATCAGCTTCC	GCGAGAAGAT	GACCATCCCC	840
GACCTGTACT	TCATCAACCT	GGCGGTGGCG	GACCTCATCC	TGGTGGCCGA	CTCCCTCATT	900
GAGGTGTTCA	ACCTGCACGA	GCGGTACTAC	GACATCGCCG	TCCTGTGCAC	CTTCATGTCT	960
CTCTTCCTGC	GGGTCAACAT	GTACAGCAGC	GTCTTCTTCC	TCACCTGGAT	GAGCTTCGAC	1020
CGCTACATCG	CCCTGGCCAG	GGCCATGCGC	TGCAGCCTGT	TCCGCACCAA	GCACCACGCC	1080
CGGCTGAGCT	GTGGCCTCAT	CTGGATGGCA	TCCGTGTCAG	CCACGCTGGT	GCCCTTCACC	1140
GCCGTGCACC	TGCAGCACAC	CGACGAGGCC	TGCTTCTGTT	TCGCGGATGT	CCGGGAGGTG	1200
CAGTGGCTCG	AGGTCACGCT	GGGCTTCATC	GTGCCCTTCG	CCATCATCGG	CCTGTGCTAC	1260
TCCCTCATTG	TCCGGGTGCT	GGTCAGGGCG	CACCGGCACC	GTGGGCTGCG	GCCCCGGCGG	1320
CAGAAGGCGC	TCCGCATGAT	CCTCGCAGTG	GTGCTGGTCT	TCTTCGTCTG	CTGGCTGCCG	1380
GAGAACGTCT	TCATCAGCGT	GCACCTCCTG	CAGCGGACGC	AGCCTGGGGC	CGCTCCTTGC	1440
AAGCAGTCTT	TCCGCCATGC	CCACCCCCTC	ACGGGCCACA	TTGTCAACCT	CGCCGCCCTC	1500
TCCAACAGCT	GCCTAAACCC	CCTCATCTAC	AGCTTTCTCG	GGGAGACCTT	CAGGGACAAG	1560
CTGAGGCTGT	ACATTGAGCA	GAAAACAAAT	TTGCCGGCCC	TGGACCGCTT	CTGTACGCT	1620
GCCCTGAAGG	CCGTCAATTCC	AGACAGCACC	GAGCAGTCGG	ATGTGAGGTT	CAGCAGTGCC	1680
GTGTAGACAG	CCTTGGCCGC	ATAGGCCCAG	CCAGGGTGTG	ACTCGGGAGC	TGCACACACC	1740
TGGGTGGACA	CAAGGCACGG	CCACGTCATG	TCTCTAAACT	GCGGTCAGAT	GTGGCTTCTG	1800
GCTCCTCGGG	CCTCGCGAGG	GTCACGCTTG	CCTGGTCACC	CTGGGGCTGC	TTAGGAAACC	1860
TCAGGACTGG	TCACCTTGCA	CTCCTCACAC	AGAATTGCTA	CAATCCCAA	GCGCTCGCCC	1920
CGCAGGGTCC	AAAGGCCAGC	GGTGACCAGC	CTGTCACCCA	GCTCCTCCCC	GCCAACCCTG	1980
CCTGCCGCTG	CACCTGCCCG	CTGCTGCAGG	AAACATTTCT	GACACCGTCG	ACCAGGAAAG	2040
CCACACGGAG	AGGCCACTGT	GGGTGAAGCG	CCTCAGTTAC	ACAGGAACCC	TAAAGCAAAT	2100
CTGCCACCGT	GGGGGAACTG	ACGCTGGAGA	TGCAAGGTGC	TGGTGGGTCT	GAGCTGGACG	2160
TCGCGGTGTG	TCCTCTGTGC	CCACGGTCTG	AGCTAGCTAG	CGCACCGCCG	AGTTAAAGAG	2220
GAGAAGGAAA	ACATGCTGCT	CTGGTGCACG	CCTGAGCGTC	CTCCATCTTC	CAGGATGGCA	2280
GCAATGGCGC	TGTGCGGCCCT	CACCAGGCCC	ACGAGGAGCA	GCAGCGCTCG	GCCCCGAGCA	2340
GCAGGAAGGC	CCCTCTGTGG	AGCGCCCCGC	GTCTGCTCCG	GGGTGGTTCA	GTCACTGCTT	2400
GTTGACATCA	ACATGGCAAT	TGCACTCATG	TGGACTGGGA	CCGTGCGAGC	TGCCGTGTGG	2460
GTTAGTCGGG	TGCCAGGACA	ATGAAATACT	CCAGCACCTG	TGGCTGACGA	ATTGTTTTCT	2520

ACAGAAGTAA CAGCTGGGGA CAACTGCGAT GATGATGTAA AAACCTTCCC ATAAAATAAG 2580
CC 2582

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 128 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGGAGGTGGG CTCCTGCTCA TCCTAGGCAT CGCACTGATT GTTACCTGTT GCAGAAAGAA 60
TAAAAATGAC ATAAGCAAAC TCATCTTCAA AAGTGGAGAT TTCCAAATGT CCCC GTATGC 120
TGAATACC 128

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 12

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TTTTTTTTTT TNG 13

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

AGCATGGCTC 10

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CACCCCTGGC ATCTTCTCCT TCC

23

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATCCTCCCCC AGTTCACCCC ATCC

24

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CCTGATAGAT GGGCACTGTG T

21

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GAACACGGCA TTGTCACTAA CT

22

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

AAGTCGCGCC CGCCCCTGAA AT

22

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GATCCCTGGC CACCGTCCGT CTGA

24

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

ACCCTGAAGT ACCCCAT

17

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

TAGAAGCATT TGCGGTG

17

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

AGATGCAGCC

10

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 12

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

TTTTTTTTTT TNA

13

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TCTCCCTCAG

10

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 12

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

TTTTTTTTTTT TNC

13

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TGGAGAGCAG

10

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

TTTATAAAG GGGTAATTCA TTA

23

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

TTAAAGCCAA TTTCAAATA AT

22

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GGTGGTGATG

10

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GGTGCGGGAA

10

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

ACATGCCGTG

10

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

ATGCCGTGTG GGTAGTC

18

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

ATTTTATGGG AAGGTTTTTA CA

22

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

AATGCGGGAG

10

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION: 12..13

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

TTTTTTTTTT TNN

13

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

TTTTTTTTTT TCC

13

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GTGACATGCC

10

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

CATGCCTGTA GAAAAAGGTT

20

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

CTTCATAGAA TCTAAGCCTA

20

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3083 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 16

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 30

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 2911

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GAATTCGGCA CGAGGMCAGG AGCTCCTTTW CTGCGTCTCC CATCATGGGG CTTAGGGTTG	60
AGTCTTCAGG TTCTGGGGGC AGGAAGGACG GGCACCTCAGG AGGCCCCCTC CCCATCCACA	120
GCCCCCTCTTT GGGAGGGGGG AAACCTGGCA ACCCGGGAGG CATGTGGATC TTTTCCTAAG	180
CAAGATGCTG AGCTGGAAAG ATGGGGGTGT AAGGTAATGT CCCAAACTGA AACTTTGCCA	240
GGCACTGGGA GAGGCTGTGA ACTCTTTTCT GGCTTTAGAA TTTAGGTCTA GATCCCCAAA	300
GGCTAAGTAC CCCCTGGGGG CTAACCAGAG GCATGCCTGG GCTGAGCTGA ACCTTCTGGT	360

GCACTGGCCC	CTGGCTGACT	GCTCTTCTGC	AGGAAGTTGG	AGGAGATTCC	TGAAGTTGAT	420
TCCTCAGGCT	GGATGTCCAA	GGGGGTTGGA	GTTTCTGATG	TCTTTCTGTC	TCCCTCTCTT	480
TTCTTTCTCT	CCCTACCAGG	TCCACTTCTT	TCAGAGGGGC	CTGCGGTGCT	CTAAAAGTTC	540
TCCTGTTAAA	GTTTAGAGCA	AATTGGTTAT	TATTTTAAAA	TCAATAAAAC	TTTTAAAAGT	600
ACTAAGACAA	CTTCTAAGAG	GGGAGTGGAC	AGAGGGCCTG	GTGGCAGCTC	ACAGTTTCTT	660
TTCTGACCTT	TGGTCTCACC	CACCAAGTGT	CCCACCTGAG	TGCCCACCTT	GCCCACCTGA	720
GGTAATGCCC	TGGGGCTCCA	CCAGTCCAGA	TCCACAGGGC	GCAGCCATGT	GGGAGTGGCG	780
GCTGATTGTT	ACCCAGTAGT	GTTGATAGCA	CATTATTTCAT	AACAGCCAAA	GAGAGGAAGC	840
AACCCAAATG	TCCATTAGCT	GATAAATGGA	TAAATGAAAT	ATGGTACGTC	CGAAGAATGG	900
AATATCATTC	ACCCATGAAA	AAGAACGAAG	TCCAGCACCA	AAACGTGCTA	CAACATGGAT	960
GAACTTCGAT	GACTTTGTGC	CACATGAAAG	AAGAAGCCAG	CCACAAAAGG	CCATATATTG	1020
TATGAAATGA	AATGTCCAGA	ATGGGCAAAAC	CCATAGAGAC	ACAAAAATCT	CCGCCACCTC	1080
CCTACTCTCG	GCTGTCTCCT	CGCGACGAGT	ACAAGCCACT	GGATCTGTCC	GATTCCACAT	1140
TGTCTTACAC	TGAAACGGAG	GCTACCAACT	CCCTCATCAC	TGCTCCGGGT	GAATTCTCAG	1200
ACGCCAGCAT	GTCTCCGGAC	GCCACCAAGC	CGAGCCACTG	GTGCAGCGTG	GCGTACTGGG	1260
AGCACCGGAC	GCGCGTGGGC	CGCTCTATG	CGGTGTACGA	CCAGGCCGTC	AGCATCTTCT	1320
ACGACCTACC	TCAGGGCAGC	GGCTTCTGCC	TGGGCCAGCT	CAACCTGGAG	CAGCGCAGCG	1380
AGTCGGTGCG	GCGAACGCGC	AGCAAGATCG	GCTTCGGCAT	CCTGCTCAGC	AAGGAGCCCC	1440
ACGGCGTGTG	GGCCTACAAC	CGCGGCGAGC	ACCCCATCTT	CGTCAACTCC	CCGACGCTGG	1500
ACGCGCCCGG	CGGCCGCGCC	CTGGTCGTGC	GCAAGGTGCC	CCCCGGCTAC	TCCATCAAGG	1560
TGTTCGACTT	CGAGCGCTCG	GGCCTGCAGC	ACGCGCCCGA	GCCCCGACGC	GCCGACGGCC	1620
CCTACGACCC	CAACAGCGTC	CGCATCAGCT	TCGCCAAGGG	CTGGGGGCCC	TGCTACTCCC	1680
GGCAGTTCAT	CACCTCCTGC	CCCTGCTGGC	TGGAGATCCT	CCTCAACAAC	CCCAGATAGT	1740
GGCGGCCCCG	GCGGGAGGGG	CGGGTGGGAG	GCCGCGGCCA	CCGCCACCTG	CCGGCCTCGA	1800
GAGGGGCCGA	TGCCCAGAGA	CACAGCCCCC	ACGGACAAAA	CCCCCCAGAT	ATCATCTACC	1860
TAGATTTAAT	ATAAAGTTTT	ATATATTATA	TGGAAATATA	TATTATACTT	GTAATTATGG	1920
AGTCATTTTT	ACAATGTAAT	TATTTATGTA	TGGTGCAATG	TGTGTATATG	GACAAAACAA	1980
GAAAGACGCA	CTTTGGCTTA	TAATTCCTTC	AATACAGATA	TATTTTCTTT	CTCTTCCTCC	2040
TTCTCTTCC	TTACTTTTTA	TATATATATA	TAAAGAAAAT	GATACAGCAG	AGCTAGGTGG	2100
AAAAGCCTGG	GTTTGGTGTA	TGGTTTTTGA	GATATTAATG	CCCAGACAAA	AAGCTAATAC	2160
CAGTCACTCG	ATAATAAAGT	ATTCGCATTA	TAGTTTTTTT	TAAACTGTCT	TCTTTTTTACA	2220
AAGAGGGGCA	GGTAGGGCTT	CAGCGGATTT	CTGACCCATC	ATGTACCTTG	AAACTTGACC	2280
TCAGTTTCA	AGTTTTACTT	TTATTGGATA	AAGACAGAAC	AAATTGAAAA	GGGAGGAAAG	2340
TCACATTAC	TCTTAAGTAA	ACCAGAGAAA	GTTCTGTTGT	TCCTTCCTGC	CCATGGCTAT	2400

GGGGTGTCCA GTGGATAGGG ATGGCGGTGG GGAAAAGGAG AATACACTGG CCATTTATCC 2460
TGGACAAGCT CTTCCAGTCT GATGGAGGAG GTTCATGCCC TAGCCTAGAA AGGCCCAGGT 2520
CCATGACCCC CATCTTTGAG TTATGAGCAA GCTAAAAGAA GACACTATTT CTCACCATTT 2580
TGTGGAAATG GCCTGGGGAA CAAAGACTGA AATGGGCCTT GAGCCCACCT GCTACCTTGC 2640
AGAGAACCAT CTCGAGCCCC GTAGATCTTT TTAGGACCTC CACAGGCTAT TTCCCACCCC 2700
CCAGCCAAAA ATAGCTCAGA ATCTGCCCAT CCAGGGCTGT ATTAATGATT TATGTAAAGG 2760
CAGATGGTTT ATTTCTACTT TGTAAGAGG AAAAGTTGAG GTTCTGGAAG GATAAATGAT 2820
TTGCTCATGA GACAAAATCA AGGTTAGAAG TTACATGGAA TTGTAGGACC AGAGCCATAT 2880
CATTAGATCA GCTTTCTGAA GAATATTCTC MAAAAAAGAA AGTCTCCTTG GCCAGATAAC 2940
TAAGAGGAAT GTTTCATTGT ATATCTTTTT TCTTGGAGAT TTATATTAAC ATATTAAGTG 3000
CTCTGAGAAG TCCTGTGTAT TATCTCTTGC TGCATAATAA ATTATCCCCA AACTTAAAAA 3060
AAAAAAAAAA AAAAAAACTC GAG 3083

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 235 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Met	Ser	Arg	Met	Gly	Lys	Pro	Ile	Glu	Thr	Gln	Lys	Ser	Pro	Pro	Pro	15
1				5					10							
Pro	Tyr	Ser	Arg	Leu	Ser	Pro	Arg	Asp	Glu	Tyr	Lys	Pro	Leu	Asp	Leu	30
			20					25					30			
Ser	Asp	Ser	Thr	Leu	Ser	Tyr	Thr	Glu	Thr	Glu	Ala	Thr	Asn	Ser	Leu	45
			35				40					45				
Ile	Thr	Ala	Pro	Gly	Glu	Phe	Ser	Asp	Ala	Ser	Met	Ser	Pro	Asp	Ala	60
			50			55					60					
Thr	Lys	Pro	Ser	His	Trp	Cys	Ser	Val	Ala	Tyr	Trp	Glu	His	Arg	Thr	80
					70					75						
Arg	Val	Gly	Arg	Leu	Tyr	Ala	Val	Tyr	Asp	Gln	Ala	Val	Ser	Ile	Phe	95
				85				90						95		
Tyr	Asp	Leu	Pro	Gln	Gly	Ser	Gly	Phe	Cys	Leu	Gly	Gln	Leu	Asn	Leu	110
			100					105					110			
Glu	Gln	Arg	Ser	Glu	Ser	Val	Arg	Arg	Thr	Arg	Ser	Lys	Ile	Gly	Phe	125
			115				120					125				
Gly	Ile	Leu	Leu	Ser	Lys	Glu	Pro	Asp	Gly	Val	Trp	Ala	Tyr	Asn	Arg	140
			130			135					140					
Gly	Glu	His	Pro	Ile	Phe	Val	Asn	Ser	Pro	Thr	Leu	Asp	Ala	Pro	Gly	

The figure consists of 12 small, vertically stacked line drawings of a man's face, labeled 1 through 12. The drawings show a progression of facial hair growth. Drawing 1 is clean-shaven. Drawing 2 shows light stubble. Drawing 3 shows more pronounced stubble. Drawing 4 shows a thin mustache and light beard. Drawing 5 shows a thin mustache and light beard. Drawing 6 shows a thin mustache and light beard. Drawing 7 shows a thin mustache and light beard. Drawing 8 shows a thin mustache and light beard. Drawing 9 shows a thin mustache and light beard. Drawing 10 shows a thin mustache and light beard. Drawing 11 shows a thin mustache and light beard. Drawing 12 shows a thin mustache and light beard.

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 375 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

-150-

Phe	Thr	Ala	Val	His	Leu	Gln	His	Thr	Asp	Glu	Ala	Cys	Phe	Cys	Phe
		195					200					205			
Ala	Asp	Val	Arg	Glu	Val	Gln	Trp	Leu	Glu	Val	Thr	Leu	Gly	Phe	Ile
	210					215					220				
Val	Pro	Phe	Ala	Ile	Ile	Gly	Leu	Cys	Tyr	Ser	Leu	Ile	Val	Arg	Val
225					230					235					240
Leu	Val	Arg	Ala	His	Arg	His	Arg	Gly	Leu	Arg	Pro	Arg	Arg	Gln	Lys
				245					250					255	
Ala	Leu	Arg	Met	Ile	Leu	Ala	Val	Val	Leu	Val	Phe	Phe	Val	Cys	Trp
			260					265					270		
Leu	Pro	Glu	Asn	Val	Phe	Ile	Ser	Val	His	Leu	Leu	Gln	Arg	Thr	Gln
		275					280					285			
Pro	Gly	Ala	Ala	Pro	Cys	Lys	Gln	Ser	Phe	Arg	His	Ala	His	Pro	Leu
	290					295					300				
Thr	Gly	His	Ile	Val	Asn	Leu	Ala	Ala	Phe	Ser	Asn	Ser	Cys	Leu	Asn
305					310					315					320
Pro	Leu	Ile	Tyr	Ser	Phe	Leu	Gly	Glu	Thr	Phe	Arg	Asp	Lys	Leu	Arg
				325					330					335	
Leu	Tyr	Ile	Glu	Gln	Lys	Thr	Asn	Leu	Pro	Ala	Leu	Asp	Arg	Phe	Cys
			340					345					350		
His	Ala	Ala	Leu	Lys	Ala	Val	Ile	Pro	Asp	Ser	Thr	Glu	Gln	Ser	Asp
		355					360					365			
Val	Arg	Phe	Ser	Ser	Ala	Val									
	370					375									